

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

## Om nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:45:23 ; Search time 150 Seconds  
Perfect score: 34 ; (without alignments)  
Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries  
Database :

1: Issued Patents NA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq: \*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq: \*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq: \*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq: \*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq: \*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq: \*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTRS\_COMB.seq: \*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq: \*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RB\_COMB.seq: \*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfilesl.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	34	US-09-874-601-100 Sequence 100, App
2	27	79.4	32	US-09-874-601-101 Sequence 101, App
3	27	79.4	34	US-09-874-601-98 Sequence 98, App
4	26	76.5	34	US-09-874-601-92 Sequence 92, App
5	26	76.5	34	US-09-874-601-93 Sequence 93, App
6	26	76.5	34	US-09-874-601-99 Sequence 99, App
7	25	73.5	34	US-09-874-601-91 Sequence 91, App
8	25	73.5	34	US-09-874-601-95 Sequence 95, App
9	25	73.5	34	US-09-874-601-96 Sequence 96, App
10	25	73.5	34	US-09-874-601-97 Sequence 97, App
11	25	55.9	34	US-09-874-601-94 Sequence 94, App
12	19	55.9	3	US-09-874-601-94 Sequence 3, App
c	13	44.1	333	US-09-482-0391-3537 Sequence 3537, App
14	15	44.1	601	US-09-949-016-81813 Sequence 81813, App
15	15	44.1	1152	US-09-045-186-1 Sequence 1, App
16	15	44.1	152	US-09-045-186-3 Sequence 2, App
17	15	44.1	1318	PCT-US93-05039-2 Sequence 1, App
18	15	44.1	1534	PCT-US93-05039-1 Sequence 1, App
19	15	44.1	1605	US-09-677-970-1 Sequence 1, App
20	15	44.1	1605	US-09-677-972B-1 Sequence 1231, App
21	15	44.1	1605	US-09-016-434-1231 Sequence 1, App
22	15	44.1	1605	US-09-677-941A-1 Sequence 3, App
23	44.1	1605	3	US-10-013-846-3 Sequence 3, App

RESULT 1  
US-09-874-601-100  
; Sequence 100, Application US/09874601  
; Patent No. 6632057  
; GENERAL INFORMATION:  
; APPLICANT: LEWIN, ALFRED S.  
; APPLICANT: SHAW, LYNN C.  
; APPLICANT: GRANT, MARIA B.  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS  
; TITL OF INVENTION: THE TREATMENT OF RETINAL DISEASES  
; FILE REFERENCE: 4300\_0.14100  
; CURRENT APPLICATION NUMBER: US/09/874, 601  
; CURRENT FILING DATE: 2001-05-01  
; PRIORITY NUMBER: 09/063, 667  
; PRIORITY FILING DATE: 1998-04-21  
; PRIORITY FILING DATE: 1997-05-09  
; PRIORITY APPLICATION NUMBER: 60/044, 492  
; PRIORITY FILING DATE: 1997-04-21  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 100  
; LENGTH: 34  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1..7)  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
; OTHER INFORMATION: OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
Query Match Similarity 100.0%; Score 34; DB 3; Length 34;  
Best Local Similarity 100.0%; Score 34; DB 3; Length 34;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 UGCAACATGAGGCCGTCGCGCGAAACGAG 34  
Db 1 UGCAACATGAGGCCGTCGCGCGAAACGAG 34  
RESULT 2  
US-09-874-601-101  
; Sequence 101, Application US/09874601  
; PATENT NO. 6632057  
; GENERAL INFORMATION:  
; APPLICANT: LEWIN, ALFRED S.

APPLICANT: SHAW, LYNN C.  
 APPLICANT: GRANT, MARIA B.  
 TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES  
 FILE REFERENCE: 4300\_014100  
 CURRENT APPLICATION NUMBER: US/09/874,601  
 CURRENT FILING DATE: 2001-05-01  
 PRIORITY APPLICATION NUMBER: 09/063,667  
 PRIOR FILING DATE: 1998-04-21  
 PRIORITY APPLICATION NUMBER: 60/046,147  
 PRIOR FILING DATE: 1997-05-09  
 PRIORITY APPLICATION NUMBER: 60/044,492  
 PRIORITY FILING DATE: 1997-04-21  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 101  
 LENGTH: 32  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: ()..()  
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 US-09-874-601-101

Query Match 79.4%; Score 27; DB 3; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAUGAGCCGUUCGGCGGAAACG 31  
 Db 3 AACUGAUGAGCCGUUCGGCGGAAAC 29

RESULT 3

SEQUENCE 98, Application US/09874601  
 Patent No. 6632057  
 GENERAL INFORMATION:  
 APPLICANT: LEWIN, ALFRED S.  
 APPLICANT: SHAW, LYNN C.  
 APPLICANT: GRANT, MARIA B.  
 TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
 FILE REFERENCE: 4300\_014100  
 CURRENT APPLICATION NUMBER: US/09/874,601  
 CURRENT FILING DATE: 2001-05-01  
 PRIORITY APPLICATION NUMBER: 09/063,667  
 PRIOR FILING DATE: 1998-04-21  
 PRIORITY APPLICATION NUMBER: 60/046,147  
 PRIOR FILING DATE: 1997-05-09  
 PRIORITY APPLICATION NUMBER: 60/044,492  
 PRIORITY FILING DATE: 1997-04-21  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 98  
 LENGTH: 34  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: ()..()  
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 US-09-874-601-98

Query Match 79.4%; Score 27; DB 3; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAUGAGCCGUUCGGCGGAAACG 31  
 Db 5 AACUGAUGAGCCGUUCGGCGGAAACG 31

RESULT 4

SEQUENCE 92, Application US/09874601  
 Patent No. 6632057  
 GENERAL INFORMATION:  
 APPLICANT: LEWIN, ALFRED S.  
 APPLICANT: SHAW, LYNN C.  
 APPLICANT: GRANT, MARIA B.  
 TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS  
 FILE REFERENCE: 4300\_014100  
 CURRENT FILING DATE: 2001-05-01  
 PRIORITY APPLICATION NUMBER: 09/063,667  
 PRIOR FILING DATE: 1998-04-21  
 PRIORITY APPLICATION NUMBER: 60/046,147  
 PRIOR FILING DATE: 1997-05-09  
 PRIORITY APPLICATION NUMBER: 60/044,492  
 PRIORITY FILING DATE: 1997-04-21  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 92  
 LENGTH: 34  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: ()..()  
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 US-09-874-601-92

Query Match 76.5%; Score 26; DB 3; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAUGAGCCGUUCGGCGAAC 30  
 Db 5 AACUGAUGAGCCGUUCGGCGAAC 30

RESULT 5

SEQUENCE 93, Application US/09874601  
 Patent No. 6632057  
 GENERAL INFORMATION:  
 APPLICANT: LEWIN, ALFRED S.  
 APPLICANT: SHAW, LYNN C.  
 APPLICANT: GRANT, MARIA B.  
 TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS  
 FILE REFERENCE: 4300\_014100  
 CURRENT APPLICATION NUMBER: US/09/874,601  
 CURRENT FILING DATE: 2001-05-01  
 PRIORITY APPLICATION NUMBER: 09/063,667  
 PRIOR FILING DATE: 1998-04-21  
 PRIORITY APPLICATION NUMBER: 60/046,147  
 PRIOR FILING DATE: 1997-05-09  
 PRIORITY APPLICATION NUMBER: 60/044,492  
 PRIORITY FILING DATE: 1997-04-21  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 93  
 LENGTH: 34  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: ()..()  
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 US-09-874-601-93

Query Match 76.5%; Score 26; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAUGAGCCGAGUCCGGGAAC 30  
 Db 5 AACUGAUGAGCCGAGUCCGGGAAC 30

RESULT 6

; Sequence 99, Application US/09874601  
 ; Patent No. 6632057

; GENERAL INFORMATION:  
 ; APPLICANT: LEWIN, ALFRED S.  
 ; APPLICANT: SHAW, LYNN C.  
 ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
 ; FILE REFERENCE: 4300\_014100  
 ; CURRENT APPLICATION NUMBER: US/09/874,601  
 ; CURRENT FILING DATE: 2001-05-01  
 ; PRIOR APPLICATION NUMBER: 09/063,667  
 ; PRIOR FILING DATE: 1998-04-21  
 ; PRIOR APPLICATION NUMBER: 60/046,147  
 ; PRIOR FILING DATE: 1997-05-09  
 ; PRIOR APPLICATION NUMBER: 60/044,492  
 ; PRIOR FILING DATE: 1997-04-21  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 99  
 ; LENGTH: 34  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1..7)  
 ; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 ; US-09-874-601-99

Query Match Local Similarity 100.0%; Score 26; DB 3; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-05; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAUGAGCCGAGUCCGGGAAC 30  
 Db 5 AACUGAUGAGCCGAGUCCGGGAAC 30

RESULT 7

; Sequence 90, Application US/09874601  
 ; Patent No. 6632057

; GENERAL INFORMATION:  
 ; APPLICANT: LEWIN, ALFRED S.  
 ; APPLICANT: SHAW, LYNN C.  
 ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
 ; FILE REFERENCE: 4300\_014100  
 ; CURRENT APPLICATION NUMBER: US/09/874,601  
 ; CURRENT FILING DATE: 2001-05-01  
 ; PRIOR APPLICATION NUMBER: 09/063,667  
 ; PRIOR FILING DATE: 1998-04-21  
 ; PRIOR APPLICATION NUMBER: 60/046,147  
 ; PRIOR FILING DATE: 1997-05-09  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 90  
 ; LENGTH: 34  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence

RESULT 8

; Sequence 91, Application US/09874601  
 ; Patent No. 6632057

; GENERAL INFORMATION:  
 ; APPLICANT: LEWIN, ALFRED S.  
 ; APPLICANT: SHAW, LYNN C.  
 ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
 ; FILE REFERENCE: 4300\_014100  
 ; CURRENT APPLICATION NUMBER: US/09/874,601  
 ; CURRENT FILING DATE: 2001-05-01  
 ; PRIOR APPLICATION NUMBER: 09/063,667  
 ; PRIOR FILING DATE: 1998-04-21  
 ; PRIOR APPLICATION NUMBER: 60/046,147  
 ; PRIOR FILING DATE: 1997-05-09  
 ; PRIOR APPLICATION NUMBER: 60/044,492  
 ; PRIOR FILING DATE: 1997-04-21  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 91  
 ; LENGTH: 34  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1..7)  
 ; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 ; US-09-874-601-91

Query Match Local Similarity 100.0%; Score 25; DB 3; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-05; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACTUGAUGAGCCGAGUCCGGGAAC 30  
 Db 6 ACUGAUGAGCCGAGUCCGGGAAC 30

RESULT 9

; Sequence 95, Application US/09874601  
 ; Patent No. 6632057

; GENERAL INFORMATION:  
 ; APPLICANT: LEWIN, ALFRED S.  
 ; APPLICANT: SHAW, LYNN C.  
 ; APPLICANT: GRANT, MARIA B.  
 ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
 ; FILE REFERENCE: 4300\_014100  
 ; CURRENT APPLICATION NUMBER: US/09/874,601  
 ; CURRENT FILING DATE: 2001-05-01  
 ; PRIOR APPLICATION NUMBER: 09/063,667  
 ; PRIOR FILING DATE: 1998-04-21  
 ; PRIOR APPLICATION NUMBER: 60/046,147  
 ; PRIOR FILING DATE: 1997-05-09  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 90  
 ; LENGTH: 34  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence

PRIOR FILING DATE: 1997-04-21  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn Version 3.0  
 SEQ ID NO: 95  
 LENGTH: 34  
 TYPE: RNA  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: ()..()  
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 US-09-874-601-95

Query Match Score 73.5%; DB 3; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACTGAUGAGCCGUTGGCGGAAC 30  
 Db 6 ACUGAUGAGCCGUTGGCGGAAC 30

RESULT 10  
 Sequence 96, Application US/09874601  
 Patent No. 6632057  
 GENERAL INFORMATION:  
 APPLICANT: LEWIN, ALFRED S.  
 APPLICANT: SHAW, LYNN C.  
 APPLICANT: GRANT, MARIA B.  
 TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
 FILE REFERENCE: 4300\_014100  
 CURRENT APPLICATION NUMBER: US/09/874,601  
 PRIOR APPLICATION NUMBER: 09/063, 667  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/046, 147  
 PRIOR FILING DATE: 1997-05-09  
 PRIOR APPLICATION NUMBER: 60/044, 492  
 PRIOR FILING DATE: 1997-04-21  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn Version 3.0  
 SEQ ID NO: 96  
 LENGTH: 34  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: ()..()  
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 US-09-874-601-96

Query Match Score 73.5%; DB 3; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACTGAUGAGCCGUTGGCGGAAC 30  
 Db 6 ACTGAUGAGCCGUTGGCGGAAC 30

RESULT 11  
 Sequence 97, Application US/09874601  
 Patent No. 6632057  
 GENERAL INFORMATION:  
 APPLICANT: LEWIN, ALFRED S.  
 APPLICANT: SHAW, LYNN C.  
 APPLICANT: GRANT, MARIA B.  
 TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
 FILE REFERENCE: 4300\_014100

RESULT 12  
 Sequence 94, Application US/09874601  
 Patent No. 6632057  
 GENERAL INFORMATION:  
 APPLICANT: LEWIN, ALFRED S.  
 APPLICANT: SHAW, LYNN C.  
 APPLICANT: GRANT, MARIA B.  
 TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD  
 FILE REFERENCE: 4300\_014100  
 CURRENT APPLICATION NUMBER: US/09/874,601  
 CURRENT FILING DATE: 2001-05-01  
 PRIOR APPLICATION NUMBER: 09/063, 667  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/046, 147  
 PRIOR FILING DATE: 1997-05-09  
 PRIOR APPLICATION NUMBER: 60/044, 492  
 PRIOR FILING DATE: 1997-04-21  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: PatentIn Version 3.0  
 SEQ ID NO: 94  
 LENGTH: 34  
 TYPE: RNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: ()..()  
 OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 US-09-874-601-94

Query Match Score 55.9%; DB 3; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GACCGCUGGCGCGGAAC 30  
 Db 12 GACCGCUGGCGCGGAAC 30

RESULT 13  
 Sequence 3537, Application US/09489039A  
 Patent No. 6610836

```

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2/09/2004/001
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US/09/489,039A
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3537
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-3537

Query Match Score 15; DB 3; Length 333;
Best Local Similarity 44.1%; Score 15; DB 3; Length 333;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 15 CCGATCGGGGAA 29
Db 62 CCGTCCGGGGAA 48

RESULT 14
US-09-49-016-81813
; Sequence 81813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et. al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81813
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-81813

Query Match Score 15; DB 3; Length 601;
Best Local Similarity 80.0%; Pred. No. 26; Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 1 UGCAGAACUGAUGC 15
Db 41 TGCAAACTGATGASC 55

RESULT 15
US-09-045-186-1
; Sequence 1, Application US/09045186
; Patent No. 6087154
; GENERAL INFORMATION:
; APPLICANT: Baez, Melvyn
; APPLICANT: Catte, Carolyn A.
; TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: 111 Corporate Center
; CITY: Indianapolis
; STATE: Indiana

```

COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/045,186  
APPLICATION NUMBER: US/09/045,186  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: P-11376  
TELEPHONE: (317) 276-3861  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1152 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1152  
US-09-045-186-1

Query Match Score 15; DB 3; Length 1152;
Best Local Similarity 73.3%; Pred. No. 26; Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 6 ACUGAUAGGCCGUUC 20
Db 538 ACTGATGAGCCGTC 552

Search completed: August 28, 2006, 10:29:28  
Job time : 154 sec

**This Page Blank (uspro,**





PT A recombinant adeno-associated virus-vectored ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. PT retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.

PS Claim 1; Page 80; 115pp; English.

The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, iNOS, RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha v; (b) a vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal degeneration. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention

SQ Sequence 34 BP; 7 A; 10 C; 13 G; 0 T; 4 U; 0 Other;

Query Match 79.4%; Score 27; DB 10; Length 34;  
Best Local Similarity 100.0%; Pred. No. 4.7e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAUGAGCCauucggcgccAAAC 31  
Db 5 AACUGAUGAGCCauucggcgccAAAC 31

RESULT 4

ABZ72857  
ID ABZ72857 standard; RNA; 34 BP.

XX AC ABZ72857;

XX DT 09-APR-2003 (first entry)

XX DB Alpha 3 Rz1 exemplary ribozyme construct SEQ ID NO:92.

XX Alpha 3 Rz1 exemplary ribozyme construct SEQ ID NO:92.

XX KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV; KW diabetich retinopathy; macular degeneration; autosomal dominant retinitis; KW blood-retinal barrier; dysfunction; adeno-associated virus; blindness; ss. OS Synthetic.

XX PN WO200288320-A2.

XX PD 07-NOV-2002.  
XX OS Synthetic.  
XX PP 01-MAY-2002; 2002WO-US013679.  
XX PR 01-MAY-2001; 2001US-00847601.  
XX PA (UFL ) UNIV FLORIDA.

XX PI Lewin AS, Shaw LC, Grant MB;  
XX WPI; 2003-111880/10.

PS Claim 1; Page 80; 115pp; English.

The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, iNOS, RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha v; (b) a vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal degeneration. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention

SQ Sequence 34 BP; 10 A; 8 C; 10 G; 0 T; 6 U; 0 Other;

Query Match 76.5%; Score 26; DB 10; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.00016; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAUGAGCCauucggcgccAAAC 30  
Db 5 AACUGAUGAGCCauucggcgccAAAC 30

RESULT 5

ABZ72858  
ID ABZ72858 standard; RNA; 34 BP.

XX AC ABZ72858;

XX DT 09-APR-2003 (first entry)

XX DB Alpha 3 Rz2 exemplary ribozyme construct SEQ ID NO:93.

XX KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV; KW diabetich retinopathy; macular degeneration; autosomal dominant retinitis; KW blood-retinal barrier; dysfunction; adeno-associated virus; blindness; ss. OS Synthetic.

XX PN WO200288320-A2.

XX PD 07-NOV-2002.  
XX OS Synthetic.  
XX PP 01-MAY-2002; 2002WO-US013679.  
XX PR 01-MAY-2001; 2001US-00847601.  
XX PA (UFL ) UNIV FLORIDA.

PP 01-MAY-2002; 2002MO-US013679.  
 XX PN  
 PR 01-MAY-2001; 2001US-00847601.  
 XX PD 07-NOV-2002.  
 PA (UYFL ) UNIV FLORIDA.  
 XX PP 01-MAY-2002; 2002MO-US013679.  
 PR 01-MAY-2001; 2001US-00847601..  
 XX PA (UYFL ) UNIV FLORIDA.  
 XX PI Lewin AS, Shaw LC, Grant MB;  
 DR WPI; 2003-111880/10.  
 PT A recombinant adeno-associated virus-vectored ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.  
 XX PS Claim 1; Page 80; 115pp; English.  
 CC The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, iNOS, RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 5, or integrin alpha V; (b) a vector comprising a polynucleotide encoding the ribozyme, where the vector is operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) can be used for treating a disease or be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal degeneration. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention  
 XX SQ sequence 34 BP; 8 A; 8 C; 13 G; 0 T; 5 U; 0 Other;  
 Query Match Best Local Similarity 76.5%; Score 26; DB 10; Length 34; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 AACUGAUGGACGCCGCGCGACGAAC 30  
 Db 5 AACUGAUGGACGCCGCGCGACGAAC 30  
 RESULT 6  
 ID ABZ72873 standard; RNA; 34 BP.  
 XX AC ABZ72873;  
 XX DT 09-APR-2003 (first entry)  
 XX DR VEGFR2 R2 exemplary ribozyme construct SEQ ID NO:14.  
 XX KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV; diabetic retinopathy; macular degeneration; autosomal dominant retinitis; blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss. OS Synthetic.

XX AC ABZ72864;  
 XX ID ABZ72864 standard; RNA; 34 BP.  
 XX AC ABZ72864;  
 XX DT 09-APR-2003 (first entry)  
 XX DE Alpha V R2 exemplary ribozyme construct SEQ ID NO:99.  
 XX KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

XX AC ABZ72864-A2.  
 XX ID WO200288320-A2.  
 XX PR 01-MAY-2002; 2002MO-US013679.  
 XX PD 07-NOV-2002.  
 XX PP 01-MAY-2002; 2002MO-US013679.  
 PR 01-MAY-2001; 2001US-00847601..  
 XX PA (UYFL ) UNIV FLORIDA.  
 XX PI Lewin AS, Shaw LC, Grant MB;  
 DR WPI; 2003-111880/10.  
 PT A recombinant adeno-associated virus-vectored ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.  
 XX PS Claim 1; Page 81; 115pp; English.  
 CC The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, iNOS, RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a vector comprising a polynucleotide encoding the ribozyme, where the vector is operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal degeneration. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention  
 XX SQ sequence 34 BP; 10 A; 7 C; 9 G; 0 T; 8 U; 0 Other;  
 Query Match Best Local Similarity 76.5%; Score 26; DB 10; Length 34; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 AACUGAUGGACGCCGCGCGACGAAC 30  
 Db 5 AACUGAUGGACGCCGCGCGACGAAC 30  
 RESULT 7  
 ID ABZ72864  
 XX AC ABZ72864;  
 XX DT 09-APR-2003 (first entry)  
 XX DE Alpha V R2 exemplary ribozyme construct SEQ ID NO:99.  
 XX KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;  
 KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;  
 KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.  
 XX Synthetic.

XX WO2002028320-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-US013679.

XX PR 01-MAY-2001; 2001US-00847601.

XX PA (UFL ) UNIV FLORIDA.

XX PT Lewin AS, Shaw LC, Grant MB;

XX DR WPI; 2003-111880/10.

PS Claim 1; Page 80; 115pp; English.

CC The present invention describes a recombinant adeno-associated virus  
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,  
 CC polypeptide, or peptide selected from the group of rod opsin, INOS,  
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a  
 CC vector comprising a polynucleotide encoding the ribozyme, where the  
 CC promoter that directs expression of the polynucleotide is operably  
 CC positioned downstream of at least a first  
 CC mammalian cell transformed with the vector; (c) a viral particle  
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector  
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell  
 CC comprising the ribozyme or the polynucleotide. Also described is a method  
 CC for decreasing the amount of mRNA encoding a selected polynucleotide in a  
 CC retinal cell of a mammalian eye, comprising providing to the eye the  
 CC composition described above, and for a time effective to specifically  
 CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can  
 CC be used in gene therapy. (I) can also be useful for treating a disease or  
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal  
 CC degeneration. (diabetic) retinopathy, or (age-related) macular  
 CC degeneration. (I) is also useful for manufacturing a medicament for  
 CC treating the diseases mentioned above, including autosomal dominant  
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful  
 CC for treating, decreasing the severity, or ameliorating the symptoms of a  
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,  
 CC blindness, a reduction in central or peripheral vision, or a reduction in  
 CC total vision. ABZ72763 to ABZ72953 represent sequences used in the  
 CC exemplification of the present invention

XX Sequence 34 BP; 9 A; 8 C; 11 G; 0 T; 6 U; 0 Other;

Query Match 76.5%; Score 26; DB 10; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.00016; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACTUGAUGAGCCGCGCUCGGCGGAAC 30  
 ID ABZ72872 standard; RNA; 34 BP.

DB 5 ACTUGAUGAGCCGCGCUCGGCGGAAC 30  
 AC ABZ72872;

XX RESULT 8  
 ABZ72872  
 XX  
 AC  
 XX

DT 09-APR-2003 (first entry)

XX DE VEGFR2 Rz1 exemplary ribozyme construct SEQ ID NO:113.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

XX KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;  
 KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;  
 KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.  
 XX Synthetic.

XX OS

XX WO2002028320-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-US013679.

XX PR 01-MAY-2001; 2001US-00847601.

XX PA (UFL ) UNIV FLORIDA.

XX PT Lewin AS, Shaw LC, Grant MB;

XX DR WPI; 2003-111880/10.

PS Claim 1; Page 81; 115pp; English.

CC The present invention describes a recombinant adeno-associated virus  
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,  
 CC polypeptide, or peptide selected from the group of rod opsin, INOS,  
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a  
 CC vector comprising a polynucleotide encoding the ribozyme, where the  
 CC promoter that directs expression of the polynucleotide is operably  
 CC positioned downstream of at least a first  
 CC mammalian cell transformed with the vector; (c) a viral particle  
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector  
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell  
 CC comprising the ribozyme or the polynucleotide. Also described is a method  
 CC for decreasing the amount of mRNA encoding a selected polypeptide in a  
 CC retinal cell of a mammalian eye, comprising providing to the eye the  
 CC composition described above, and for a time effective to specifically  
 CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can  
 CC be used in gene therapy. (I) can also be used for treating a disease or  
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal  
 CC degeneration. (diabetic) retinopathy, or (age-related) macular  
 CC degeneration. (I) is also useful for manufacturing a medicament for  
 CC treating the diseases mentioned above, including autosomal dominant  
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful  
 CC for treating, decreasing the severity, or ameliorating the symptoms of a  
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,  
 CC blindness, a reduction in central or peripheral vision, or a reduction in  
 CC total vision. ABZ72763 to ABZ72953 represent sequences used in the  
 CC exemplification of the present invention

XX Sequence 34 BP; 10 A; 9 C; 10 G; 0 T; 5 U; 0 Other;

Query Match 76.5%; Score 26; DB 10; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.00016; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACTUGAUGAGCCGCGCUCGGCGGAAC 30  
 DB 5 ACTUGAUGAGCCGCGCUCGGCGGAAC 30  
 AC  
 XX RESULT 9

Query Match	73-5%; Score 25;	DB 10;	Length 34;
Best Local Similarity	100.0%;	Pred. No.	0.00058;
Matches	25;	Conservative	0;
OY		Mismatches	0;
	6 ACTUGAUGACCGGUNGCGCGGGAAAC	Indices	0;
	30	Gaps	0;

C C total vision. ABZ2763 to ABZ2793 represent sequences used in the exemplification of the present invention

Query Match		73.5%;	Score 25;	DB 10;	Length 34;
Best Local Similarity		100.0%;	Pred. No. 0.00058;		
Matches		25;	Conservative	0;	Mismatches 0;
Y	6 ACTUGAUGAGCCGCGUCGGCGAAC 30				
b	6 ACTUGAUGAGCCGCGUCGGCGAAC 30				
<b>RESULT 11</b>					
AC	ABZ72856				
CX	ABZ72856 standard; RNA; 34 BP.				
AC	ABZ72856;				
CT	09-APR-2003 (first entry)				
A2B Rz1 exemplary ribozyme construct SEQ ID NO:91.					
Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV; diabetic retinopathy; macular degeneration; autosomal dominant retinitis; blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.					
Synthetic.					
KW	W0200288320-A2.				
DD	07-NOV-2002.				
TP	01-MAY-2002; 2002WO-US013679.				
PR	01-MAY-2001; 2001US-00847601.				
RR	(UYFL ) UNIV FLORIDA.				
RC	Lewin AS, Shaw LC, Grant MB;				
CC	WPI; 2003-111880/10.				
CC	A recombinant adeno-associated virus-vectorized ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.				
CC	Claim 1; Page 80; 115pp; English.				
CC	The present invention describes a recombinant adeno-associated virus (AAV) vectorized ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, INOS, RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal dysfunction, (diabetic) retinopathy, or (age-related) macular degeneration. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in				
CC	total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention				
CC	Sequence 34 BP; 9 A; 8 C; 11 G; 0 T; 6 U; 0 Other;				
CC	Query Match 73.5%; score 25; DB 10; Length 34;				
CC	-Best Local Similarity 100.0%; Pred. No. 0.00058;				
CC	Matches 25; Conservative 0; Mismatches 0;				
Oy	6 ACTUGAUGAGCCGCGUCGGCGAAC 30				
Dy	6 ACTUGAUGAGCCGCGUCGGCGAAC 30				
<b>RESULT 12</b>					
ID	ABZ72870				
XX	ABZ72870 standard; RNA; 34 BP.				
AC	ABZ72870;				
XX	09-APR-2003 (first entry)				
XX	VEGFR1 Rz1 exemplary ribozyme construct SEQ ID NO:111.				
XX	Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; ophthalmological; gene therapy; eye; retinal dysfunction; AAV; diabetic retinopathy; macular degeneration; autosomal dominant retinitis; blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.				
XX	Synthetic.				
XX	W0200288320-A2.				
XX	07-NOV-2002.				
TP	01-MAY-2002; 2002WO-US013679.				
PR	01-MAY-2001; 2001US-00847601.				
PR	(UYFL ) UNIV FLORIDA.				
XX	Lewin AS, Shaw LC, Grant MB;				
XX	WPI; 2003-111880/10.				
PT	A recombinant adeno-associated virus-vectorized ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.				
PT	Claim 1; Page 81; 115pp; English.				
PS	The present invention describes a recombinant adeno-associated virus (AAV) vectorized ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, INOS, RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal dysfunction, (diabetic) retinopathy, or (age-related) macular degeneration. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in				
CC	total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention				
CC	Sequence 34 BP; 9 A; 8 C; 11 G; 0 T; 6 U; 0 Other;				
CC	Query Match 73.5%; score 25; DB 10; Length 34;				
CC	-Best Local Similarity 100.0%; Pred. No. 0.00058;				
CC	Matches 25; Conservative 0; Mismatches 0;				
Oy	6 ACTUGAUGAGCCGCGUCGGCGAAC 30				
Dy	6 ACTUGAUGAGCCGCGUCGGCGAAC 30				

CC treating the diseases mentioned above, including autosomal dominant  
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful  
 CC for treating, decreasing the severity, or ameliorating the symptoms of a  
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye, in  
 CC blindness, a reduction in central or peripheral vision, or a reduction in  
 CC total vision. ABZ72763 to ABZ72953 represent sequences used in the  
 exemplification of the present invention.

SQ Sequence 34 BP; 8 A; 12 C; 8 G; 0 T; 6 U; 0 Other;

Query Match Similarity 100.0%; Pred. No. 0.00058; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.00058; Length 34;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13 ABZ72860

ID ABZ72860 standard; RNA; 34 BP.  
 XX AC ABZ72860;

XX DR 09-APR-2003 (first entry)

DB Alpha 5 Rz2 exemplary ribozyme construct SEQ ID NO:95.

KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV; KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis; KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss; KW Synthetic.

OS PN WO200288320-A2.

XX PD 07-NOV-2002.

XX PR 01-MAY-2002; 2002WO-US013679.

XX DR PR 01-MAY-2001; 2001US-00847601.

XX PA (UYFL ) UNIV FLORIDA.

XX PI Lewin AS, Shaw LC, Grant MB;

XX PR XX WPI; 2003-111880/10.

PS A recombinant adeno-associated virus-vectorized ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.

XX Claim 1; Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus vectorized ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e), a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically

CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can CC be used in gene therapy. (I) can be used for treating a disease or CC dysfunction of the mammalian eye, such as a retinal disease or retinal CC dysfunction. (diabetic) retinopathy, or (age-related) macular CC degeneration. (I) is also useful for manufacturing a medicament for CC treating the diseases mentioned above, including autosomal dominant CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful CC for treating, decreasing the severity, or ameliorating the symptoms of a CC pathological condition, e.g. atrophic or pigmented lesions of the eye, in CC blindness, a reduction in central or peripheral vision, or a reduction in CC total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention.

SQ Sequence 34 BP; 8 A; 8 C; 13 G; 0 T; 5 U; 0 Other;

Query Match Similarity 100.0%; Pred. No. 0.00058; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.00058; Length 34;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14 ABZ72861

ID ABZ72861 standard; RNA; 34 BP.

XX AC ABZ72861;

XX DT 09-APR-2003 (first entry)

DB Alpha 1 Rz1 exemplary ribozyme construct SEQ ID NO:96.

KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target; KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV; KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis; KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss; KW Synthetic.

OS PN WO200288320-A2.

XX PD 07-NOV-2002.

XX PR 01-MAY-2002; 2002WO-US013679.

XX PR 01-MAY-2001; 2001US-00847601.

XX PA (UYFL ) UNIV FLORIDA.

XX PI Lewin AS, Shaw LC, Grant MB;

XX DR PR XX WPI; 2003-111880/10.

PS A recombinant adeno-associated virus-vectorized ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.

XX Claim 1; Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus vectorized ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, iNOS, RNS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a vector comprising a polynucleotide encoding the ribozyme, where the first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, iNOS, RNS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a vector comprising a polynucleotide encoding the ribozyme, where the first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, iNOS, RNS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; the vector comprising a polynucleotide encoding the ribozyme, where the polyribonucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector

comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide.

XX  
CONTINUATION OF THE HISTORY OF THE CHURCH OF ENGLAND

comprising the ribozyme or the polyuridine. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or

```

Sequence 34 or: > A; > C; > G; > T; > U; > CAAU;
Query Match          73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100%; Pred. 0.00058; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
6 ACUGAUGCAGCCGUUCGGCGGAAAC 30

```

Db 6 ACUGAUGCAGCGTUCGGCGAAC 300

RESULT 15  
AAC88594  
ID AAC88594 standard. DNA: AA BB

XX  
DT  
02-MAR-2001 (first entry)

Oligonucleotide #1 used to clone ribozyme SOD-1 295.

Ribozyme; retinal degradation; retinal disease; learning; memory; ss. amyotrophic lateral sclerosis; tumour suppression; ss.

Musae sp.

MOZUO0001.G0-NZ:

28 APR 2000: 30

30-APR-1999; 99US-0131942P.

(UYFL ) UNIV FLORIDA.

Lewin AS, Muzychka N, Haubswirth MM, Teschendorff C, Burger C,

卷之三

contracting genes with a library of ribozymes, useful for identifying genes involved in a neural disease, learning or memory, tumor

בְּמִתְּחַנֵּן כָּבֵד כָּלִיל

The present invention relates to a method for identifying a gene with a

selected function controlling genes with a small number of nucleotides and identifying at least one ribozyme that alters the selected function of

The present sequence is an oligonucleotide used in the present invention. The methods (and ribozymes) are useful for identifying novel genes.

genes involved in retinal degradation, retinal disease, learning or memory, amyotrophic lateral sclerosis, or tumour suppression, and for producing non-human animal models of diseases.

**This Page Blank (uspto)**

Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2006, 09:50:18 ; Search time 716 Second  
                   (without alignment(s))  
                   583.491 Million cell updates/sec

Title:	US-09-847-601B-100
Perfect score:	34
Sequence:	1 ugcaaacugauagccgcugcgccggaaacgaaag 34
Scoring table:	Oligo_NUC
Gapext:	60.0
Searched:	18892170 seqs, 6143817638 residues
Word size :	1
Total number of hits satisfying chosen parameters:	37781012
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing: Listing first 45 summaries	
Database :	Published Applications NA Main: *
	1: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us07_PUBCOMB.seq:*
	2: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us08_PUBCOMB.seq:*
	3: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us09_PUBCOMB.seq:*
	4: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us09C_PUBCOMB.seq:*
	5: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1A_PUBCOMB.seq:*
	6: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1B_PUBCOMB.seq:*
	7: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1C_PUBCOMB.seq:*
	8: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1D_PUBCOMB.seq:*
	9: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1E_PUBCOMB.seq:*
	10: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1F_PUBCOMB.seq:*
	11: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1G_PUBCOMB.seq:*
	12: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1H_PUBCOMB.seq:*
	13: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1I_PUBCOMB.seq:*
	14: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1J_PUBCOMB.seq:*
	15: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1K_PUBCOMB.seq:*
	16: /EMC_Celerra_SIDS3/pctodata/2/pubpna/us1L_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	34	100	0	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
2	27	79	4	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
3	27	79	4	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
4	26	76	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
5	26	76	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
6	26	76	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
7	25	73	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
8	25	73	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
9	25	73	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
10	25	73	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
11	25	73	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
12	25	73	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
13	25	73	5	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
14	16	47	1	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
15	16	47	1	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
16	16	47	1	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl
17	16	47	1	Sequence 100, App Sequence 01, App Sequence 98, Appl Sequence 92, Appl Sequence 93, Appl Sequence 99, Appl Sequence 90, Appl Sequence 91, Appl Sequence 95, Appl Sequence 96, Appl Sequence 97, Appl Sequence 94, Appl Sequence 235, Appl Sequence 3619, Appl Sequence 18859, A Sequence 5630, Appl Sequence 1, Appl

**ALIGNMENTS**

RESULT 1  
                   US-09-847-601B-100  
                   Publication No. US2005009628211  
                   ; GENERAL INFORMATION:  
                   ; APPLICANT: LEWIN, ALFRED S.  
                   ; APPLICANT: SHAW, LIND C.  
                   ; APPLICANT: GRANT, MARIA B.  
                   ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERY  
                   ; FILE REFERENCE: 4300\_04100  
                   ; CURRENT APPLICATION NUMBER: US/09/847,601B  
                   ; CURRENT FILING DATE: 2001-05-01  
                   ; PRIOR APPLICATION NUMBER: 09/063, 667  
                   ; PRIOR FILING DATE: 1998-04-21  
                   ; PRIOR APPLICATION NUMBER: 60/046, 147  
                   ; PRIOR FILING DATE: 1998-05-09  
                   ; NUMBER OF SEQ ID NOS: 182  
                   ; SOFTWARE: PatentIn version 3.2  
                   ; SBQ\_ID NO 100  
                   ; LENGTH: 34  
                   ; TYPE: RNA  
                   ; ORGANISM: Artificial  
                   ; FEATURE:  
                   ; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
                   ; US-09-847-601B-100  
                   ; Query Match Best Local Similarity 100.0%; Score 34; DB 4;  
                   ; Matches 34; Conservative 0; Mismatches 0;  
                   ; QY 1 UGCAACUGAUAGCCGUUCGGGGCGAACGAG 34  
                   ; Db 1 UGCAACUGAUAGCCGUUCGGGGCGAACGAG 34  
                   ; RESULT 2  
                   ; US-09-847-601B-101

## SUMMARIES

Sequence 100, App  
 Sequence 101, App  
 Sequence 98, Appl  
 Sequence 92, Appl  
 Sequence 93, Appl  
 Sequence 99, Appl  
 Sequence 90, Appl  
 Sequence 91, Appl  
 Sequence 95, Appl  
 Sequence 96, Appl  
 Sequence 97, Appl  
 Sequence 94, Appl  
 Sequence 322, Ap  
 Sequence 3619, Ap  
 Sequence 18859, A  
 Sequence 5630, Ap  
 Sequence 1, Appl

---

Query Match 100.0%; Score 100.0%; Pred Best Local Similarity 100.0%; Pred Matches 34; Conservative 0; Mil Oy 1 UGGAACTGAUGAGCCGTCGCGCT  
 Db 1 UGCCAACUGAUGGACCCAUUCCGCGCT  
 RESULT<sup>2</sup>  
 US-09-847-601B-100

; Sequence 101, Application US/09847601B  
; Publication No. US20050096282A1  
; GENERAL INFORMATION:  
; APPLICANT: LEWIN, ALFRED S.  
; APPLICANT: SHAW, LYNN C.  
; APPLICANT: GRANT, MARIA B.  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES  
; FILE REFERENCE: 4300.014100  
; CURRENT APPLICATION NUMBER: US/09/847,601B  
; CURRENT FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: 09/063,667  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 101  
; LENGTH: 32  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
; US-09-847-601B-101

Query Match 79.4%; Score 27; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	Db	Sequence
5	3	AACUGAUGAGCCGCGUUCGGCGAAC 31
		AACUGAUGAGCCGCGUUCGGCGAAC 29

RESULT 3  
US-09-847-601B-98

; Sequence 98, Application US/09947601B  
; Publication No. US20050096282A1  
; GENERAL INFORMATION:  
; APPLICANT: LEWIN, ALFRED S.  
; APPLICANT: SHAW, LYNN C.  
; APPLICANT: GRANT, MARIA B.  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
; FILE REFERENCE: 4300.014100  
; CURRENT APPLICATION NUMBER: US/09/847,601B  
; CURRENT FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: 09/063,667  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 98  
; LENGTH: 34  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
; US-09-847-601B-98

Query Match 79.4%; Score 27; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	Db	Sequence
5	5	AACUGAUGAGCCGCGUUCGGCGAAC 31
		AACUGAUGAGCCGCGUUCGGCGAAC 31

RESULT 4  
US-09-847-601B-92

; Sequence 92, Application US/09947601B  
; Publication No. US20050096282A1  
; GENERAL INFORMATION:  
; APPLICANT: LEWIN, ALFRED S.  
; APPLICANT: SHAW, LYNN C.  
; APPLICANT: GRANT, MARIA B.  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES  
; FILE REFERENCE: 4300.014100  
; CURRENT APPLICATION NUMBER: US/09/847,601B  
; CURRENT FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: 09/063,667  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 92  
; LENGTH: 34  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
; US-09-847-601B-92

Query Match 76.5%; Score 26; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	Db	Sequence
5	5	AACUGAUGAGCCGCGUUCGGCGAAC 30
		AACUGAUGAGCCGCGUUCGGCGAAC 30

RESULT 5  
US-09-847-601B-93

; Sequence 93, Application US/09947601B  
; Publication No. US20050096282A1  
; GENERAL INFORMATION:  
; APPLICANT: LEWIN, ALFRED S.  
; APPLICANT: SHAW, LYNN C.  
; APPLICANT: GRANT, MARIA B.  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
; FILE REFERENCE: 4300.014100  
; CURRENT APPLICATION NUMBER: US/09/847,601B  
; CURRENT FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: 09/063,667  
; PRIOR FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 93  
; LENGTH: 34  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
; US-09-847-601B-93

Query Match 76.5%; Score 26; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	Db	Sequence
5	5	AACUGAUGAGCCGCGUUCGGCGAAC 30
		AACUGAUGAGCCGCGUUCGGCGAAC 30

Db 5 |||||||ACUGAUGAGCCGCUUCGGCGGCGAAC 30

RESULT 6 Sequence 99, Application US/09847601B  
US-09-847-601B-99  
Publication No. US20050096282A1  
GENERAL INFORMATION:  
APPLICANT: LEWIN, ALFRED S.  
APPLICANT: SHAW, LYNN C.  
APPLICANT: GRANT, MARIA B.  
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
FILE REFERENCE: 4300.014100  
CURRENT APPLICATION NUMBER: US/09/847,601B  
CURRENT FILING DATE: 2001-05-01  
PRIORITY APPLICATION NUMBER: 09/063,667  
PRIORITY FILING DATE: 1997-04-21  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 99  
LENGTH: 34  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-847-601B-99

Query Match Best Local Similarity 76.5%; Score 26; DB 4; Length 34;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAUGAGCCGCUUCGGCGGCGAAC 30  
Db 5 AACUGAUGAGCCGCUUCGGCGGCGAAC 30

RESULT 7 US-09-847-601B-90

Sequence 90, Application US/09847601B  
Publication No. US20050096282A1  
GENERAL INFORMATION:  
APPLICANT: LEWIN, ALFRED S.  
APPLICANT: SHAW, LYNN C.  
APPLICANT: GRANT, MARIA B.  
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
FILE REFERENCE: 4300.014100  
CURRENT APPLICATION NUMBER: US/09/847,601B  
PRIORITY APPLICATION NUMBER: 09/063,667  
PRIORITY FILING DATE: 1997-04-21  
PRIORITY APPLICATION NUMBER: 60/046,147  
PRIORITY FILING DATE: 1998-04-21  
PRIORITY APPLICATION NUMBER: 60/044,492  
PRIORITY FILING DATE: 1997-05-09  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 91  
LENGTH: 34  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-847-601B-91

Query Match Best Local Similarity 100.0%; Score 26; DB 4; Length 34;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACTUGAUGAGCCGCUUCGGCGGCGAAC 30  
Db 6 ACUGAUGAGCCGCUUCGGCGGCGAAC 30

RESULT 8 US-09-847-601B-91

Sequence 91, Application US/09847601B  
US-09-847-601B-91  
Publication No. US20050096282A1  
GENERAL INFORMATION:  
APPLICANT: LEWIN, ALFRED S.  
APPLICANT: SHAW, LYNN C.  
APPLICANT: GRANT, MARIA B.  
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
FILE REFERENCE: 4300.014100  
CURRENT APPLICATION NUMBER: US/09/847,601B  
CURRENT FILING DATE: 2001-05-01  
PRIORITY APPLICATION NUMBER: 09/063,667  
PRIORITY FILING DATE: 1998-04-21  
PRIORITY APPLICATION NUMBER: 60/046,147  
PRIORITY FILING DATE: 1997-05-09  
PRIORITY APPLICATION NUMBER: 60/044,492  
PRIORITY FILING DATE: 1997-04-21  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 91  
LENGTH: 34  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-847-601B-95

Query Match Best Local Similarity 73.5%; Score 25; DB 4; Length 34;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACTUGAUGAGCCGCUUCGGCGGCGAAC 30  
Db 6 ACUGAUGAGCCGCUUCGGCGGCGAAC 30

RESULT 9 US-09-847-601B-95

Sequence 95, Application US/09847601B  
US-09-847-601B-95  
Publication No. US20050096282A1  
GENERAL INFORMATION:  
APPLICANT: LEWIN, ALFRED S.  
APPLICANT: SHAW, LYNN C.  
APPLICANT: GRANT, MARIA B.  
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
FILE REFERENCE: 4300.014100  
CURRENT APPLICATION NUMBER: US/09/847,601B  
CURRENT FILING DATE: 2001-05-01  
PRIORITY APPLICATION NUMBER: 09/063,667  
PRIORITY FILING DATE: 1998-04-21  
PRIORITY APPLICATION NUMBER: 60/046,147  
PRIORITY FILING DATE: 1997-05-09  
PRIORITY APPLICATION NUMBER: 60/044,492  
PRIORITY FILING DATE: 1997-04-21  
NUMBER OF SEQ ID NOS: 182  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 90  
LENGTH: 34  
TYPE: RNA  
ORGANISM: Artificial  
FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-847-601B-95

Query Match Best Local Similarity 100.0%; Score 25; DB 4; Length 34;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACTUGAUGAGCCGCUUCGGCGGCGAAC 30  
Db 6 ACUGAUGAGCCGCUUCGGCGGCGAAC 30

Query Match 73.5%; Score 25; DB 4; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	ACUGAUGAGCCGCUUCGGCGGAAC	30
Db	6	ACUGAUGAGCCGCUUCGGCGGAAC	30

RESULT 10  
 US-09-847-601B-95  
 ; Sequence 95, Application US/09847601B  
 ; Publication No. US20050096282A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEWIN, ALFRED S.  
 ; APPLICANT: SHAW, LYNN C.  
 ; APPLICANT: GRANT, MARIA B.  
 ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
 ; FILE REFERENCE: 4300.01100  
 ; CURRENT APPLICATION NUMBER: US/09-847,601B  
 ; CURRENT FILING DATE: 2001-05-01  
 ; PRIORITY NUMBER: 60/046,147  
 ; PRIORITY FILING DATE: 1997-05-09  
 ; PRIORITY APPLICATION NUMBER: 60/044,492  
 ; PRIORITY FILING DATE: 1997-04-21  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 96  
 ; LENGTH: 34  
 ; TYPE: RNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 ; US-09-847-601B-95

Query Match 73.5%; Score 25; DB 4; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	ACUGAUGAGCCGCUUCGGCGGAAC	30
Db	6	ACUGAUGAGCCGCUUCGGCGGAAC	30

RESULT 11  
 US-09-847-601B-97  
 ; Sequence 97, Application US/09847601B  
 ; Publication No. US20050096282A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEWIN, ALFRED S.  
 ; APPLICANT: SHAW, LYNN C.  
 ; APPLICANT: GRANT, MARIA B.  
 ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
 ; FILE REFERENCE: 4300.01100  
 ; CURRENT APPLICATION NUMBER: US/09-847,601B  
 ; CURRENT FILING DATE: 2001-05-01  
 ; PRIORITY NUMBER: 60/046,147  
 ; PRIORITY FILING DATE: 1997-04-21  
 ; PRIORITY APPLICATION NUMBER: 60/044,492  
 ; PRIORITY FILING DATE: 1997-04-21  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 94  
 ; LENGTH: 34  
 ; TYPE: RNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 ; US-09-847-601B-94

Query Match 55.9%; Score 19; DB 4; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.36;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	12	GACCGGCGGCGCGGAAC	30
Db	12	GACCGGCGGCGCGGAAC	30

RESULT 12  
 US-09-847-601B-94  
 ; Sequence 94, Application US/09847601B  
 ; Publication No. US20050096282A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEWIN, ALFRED S.  
 ; APPLICANT: SHAW, LYNN C.  
 ; APPLICANT: GRANT, MARIA B.  
 ; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS FOR THE TREATMENT OF RETINAL DISEASES  
 ; FILE REFERENCE: 4300.014100  
 ; CURRENT APPLICATION NUMBER: US/09-847,601B  
 ; CURRENT FILING DATE: 2001-05-01  
 ; PRIORITY NUMBER: 60/046,147  
 ; PRIORITY FILING DATE: 1998-04-21  
 ; PRIORITY APPLICATION NUMBER: 60/044,492  
 ; PRIORITY FILING DATE: 1997-05-09  
 ; PRIORITY APPLICATION NUMBER: 60/046,147  
 ; PRIORITY FILING DATE: 1997-04-21  
 ; NUMBER OF SEQ ID NOS: 182  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 94  
 ; LENGTH: 34  
 ; TYPE: RNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
 ; US-09-847-601B-97

Query Match 73.5%; Score 25; DB 4; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	ACUGAUGAGCCGCUUCGGCGGAAC	30
Db	6	ACUGAUGAGCCGCUUCGGCGGAAC	30

RESULT 13  
 US-10-437-963-3252/c  
 ; Sequence 3252, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalcik, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221,B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO: 3252  
 ; LENGTH: 463  
 ; TYPE: DNA  
 ; ORGANISM: Artificial

ORGANISM: *Oryza sativa*  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102953C.1  
; US-10-437-363-3252

Query Match Best Local Similarity 47.1%; Score 16; DB 8; Length 463;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 USCAAACGAAUGAGCC 16  
Db 221 TCGAACATGATGAGCC 206

RESULT 14  
US-10-156-761-3619  
; Sequence 3619, Application US/10156761  
; Publication No. US2003011901BA1

GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: MORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAOHISI  
APPLICANT: SAKAKI, YOSHIOUKI  
APPLICANT: HATORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 3619

LENGTH: 1845  
TYPE: DNA  
ORGANISM: *Streptomyces avermitilis*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1845)

US-10-156-761-3619

Query Match Best Local Similarity 47.1%; Score 16; DB 7; Length 1845;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCCGTTGGCGCGGA 27  
Db 352 GAGCCGTTGGCGCGGA 367

---

Search completed: August 28, 2006, 10:41:09  
Job time : 718 secs

Query Match Best Local Similarity 47.1%; Score 16; DB 8; Length 5335;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCCGTTGGCGCGGA 27  
Db 352 GAGCCGTTGGCGCGGA 367

Query Match Best Local Similarity 87.5%; Score 16; DB 8; Length 5335;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GAGCCGTTGGCGCGGA 27  
Db 352 GAGCCGTTGGCGCGGA 367

NAME/KEY: CDS  
LOCATION: (1)..(5335)

OTHER INFORMATION: unsure at all n locations  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(5335)  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_24377C.1  
US-10-437-363-18859

This Page Blank (uspiu,





NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 20318  
; LENGTH: 1243  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK099148  
; DATABASE ENTRY DATE: 2002-08-28  
; US-10-449-902-20318

Query Match      44.1%; Score 15; DB 6; Length 1243;  
Best Local Similarity 86.7%; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      2 GCAACATGAGAGCC 16  
Db      390 GCAACTCTATGAGCC 404

RESULT 6  
US-10-449-902-4455  
; Sequence 4455, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences. Institution.  
; APPLICANT: Bio-oriented Technology Research Advancement. Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: WO2-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIORITY APPLICATION NUMBER: JP 2002-203269  
; PRIORITY FILING DATE: 2002-05-30  
; PRIORITY APPLICATION NUMBER: JP 2002-383870  
; PRIORITY FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 4455  
; LENGTH: 1249  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK061781  
; DATABASE ENTRY DATE: 2001-12-06  
; US-10-449-902-4455

Query Match      44.1%; Score 15; DB 6; Length 1249;  
Best Local Similarity 86.7%; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      2 GCAACATGAGAGCC 16  
Db      405 GCAACTCTATGAGCC 419

RESULT 7  
US-11-266-748A-251890/c  
; Sequence 251890, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Hartkin, Paul  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIORITY APPLICATION NUMBER: EP 04105479.2  
; PRIORITY FILING DATE: 2004-11-03  
; PRIORITY APPLICATION NUMBER: EP 04105482.6  
; PRIORITY FILING DATE: 2004-11-03  
; PRIORITY APPLICATION NUMBER: EP 04105483.4  
; PRIORITY FILING DATE: 2004-11-03  
; PRIORITY APPLICATION NUMBER: EP 04105507.0  
; PRIORITY FILING DATE: 2004-11-03  
; PRIORITY APPLICATION NUMBER: EP 04105485.9  
; PRIORITY FILING DATE: 2004-11-03  
; PRIORITY APPLICATION NUMBER: EP 04105484.2  
; PRIORITY FILING DATE: 2004-11-03  
; PRIORITY APPLICATION NUMBER: US 60/662,276  
; PRIORITY FILING DATE: 2005-03-14  
; PRIORITY APPLICATION NUMBER: US 60/700,293  
; PRIORITY FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 433996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 312407  
; LENGTH: 1342  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; US-11-266-748A-312407

Query Match      44.1%; Score 15; DB 8; Length 1342;  
Best Local Similarity 73.3%; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;  
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY      6 ACTGGAUGAGCCGTC 20

Db 1025 ACTGATGAGCCGTC 1039

RESULT 9  
US-10-449-902-20725

; Publication No. US20060133505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20725

; LENGTH: 1551

; TYPE: DNA

; ORGANISM: Oryza sativa

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: ARK071031

; DATABASE ENTRY DATE: 2001-12-06

; US-10-449-902-20725

Query Match 44.1%; Score 15; DB 6; Length 1551;  
Best Local Similarity 86.7%; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GCGCAGUCGGGGCGAA 28  
Db 291 GCCTTCCGGGGCAA 305

RESULT 10  
US-11-256-428-61/C

; Sequence 61, Application US/11256428

; Publication No. US20060055987A1

; GENERAL INFORMATION:

; APPLICANT: NIELLETT, Charles L.

; TITLE OF INVENTION: Methods and Materials for Conferring Resistance to Pests and Time of Invention: Pathogens of Plants

; FILE REFERENCE: VEN-100

; CURRENT APPLICATION NUMBER: US/11/256,428

; CURRENT FILING DATE: 2005-10-21

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 61

; LENGTH: 1773

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Pratylenchus scribneri cDNA

; US-11-256-428-61

Query Match 44.1%; Score 15; DB 8; Length 1773;  
Best Local Similarity 80.0%; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 AUGAGCCGUUCGGG 24  
Db 72 ATAGGCCGTGCGG 58

RESULT 11  
US-11-266-748A-194170

; Sequence 184170, Application US/11266748A

Db 60/662,276

Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Milligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and FILE REFERENCE: 55115-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: US 60/662,276

; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/700,293

; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 184170

; LENGTH: 2253

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2038). (2071)

; OTHER INFORMATION: n is a, c, g, or t

; US-11-266-748A-194170

Query Match 44.1%; Score 15; DB 8; Length 2253;  
Best Local Similarity 73.3%; Pred. No. 11; Mismatches 4; Indels 0; Gaps 0;

Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACTGAUGAGCCGTC 20  
Db 796 ACTGATGAGCCGTC 810

RESULT 12  
US-11-266-748A-1941643

; Sequence 191643, Application US/11266748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Milligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and FILE REFERENCE: 55115-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14  
 PRIOR APPLICATION NUMBER: US 60/700,293  
 PRIORITY FILING DATE: 2005-07-18  
 NUMBER OF SEQ ID NOS: 433996  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 191643  
 LENGTH: 2253  
 TYPE: DNA  
 ORGANISM: Homo Sapiens  
 FEATURE:  
 NAME/KEY: m18c feature  
 LOCATION: (2038)..(2071)  
 OTHER INFORMATION: n is a, c, g, or t  
 ; US-11-266-748A-191643

Query Match Score 15; DB 8; Length 2253;  
 Best Local Similarity 73.3%; Pred. No. 11;  
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACTGAGAGCCGUC 20  
 Db 795 ACTGATGAGCCGTC 810

RESULT 13  
 US-11-226-554-73  
 ; Sequence 73, Application US/11226554  
 ; Publication No. US20060147373A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Caihns,Belinda  
 ; APPLICANT: Chen,Ruihuan  
 ; APPLICANT: Frantz,Gretchen  
 ; APPLICANT: Hillian,Kenneth J.  
 ; APPLICANT: Koeppen,Hartmut  
 ; APPLICANT: Phillip,Heidi S.  
 ; APPLICANT: Polakis,Paul  
 ; APPLICANT: Spencer,Susan D.  
 ; APPLICANT: Smith,Victoria  
 ; APPLICANT: Williams,P. Mickey  
 ; APPLICANT: Wu,Thomas D.  
 ; APPLICANT: Zhang,Zemin  
 ; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and Treatment of Tumor

FILE REFERENCE: P5001R1 US  
 CURRENT APPLICATION NUMBER: US/11/248,718  
 CURRENT FILING DATE: 2005-10-11  
 PRIOR APPLICATION NUMBER: US 10/177,488  
 PRIOR FILING DATE: 2002-06-19  
 PRIOR APPLICATION NUMBER: US 60/299,500  
 PRIOR FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: US 60/300,880  
 PRIOR FILING DATE: 2001-06-25  
 PRIOR APPLICATION NUMBER: US 60/304,813  
 PRIOR FILING DATE: 2001-07-11  
 PRIOR APPLICATION NUMBER: US 60/312,312  
 PRIOR FILING DATE: 2001-08-13  
 PRIOR APPLICATION NUMBER: US 60/314,280  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: US 60/339,227  
 PRIOR FILING DATE: 2001-10-19  
 PRIOR APPLICATION NUMBER: US 60/323,268  
 PRIOR FILING DATE: 2001-09-18  
 PRIOR APPLICATION NUMBER: US 60/336,827  
 PRIOR FILING DATE: 2001-11-07  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 154  
 SEQ ID NO 73  
 LENGTH: 2752  
 TYPE: DNA  
 ORGANISM: Homo Sapiens  
 US-11-248-718-73

Query Match Score 15; DB 9; Length 2752;  
 Best Local Similarity 73.3%; Pred. No. 11;  
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACTGAGAGCCGUC 20  
 Db 746 ACTGATGAGCCGTC 760

RESULT 15  
 US-11-266-748A-29125  
 ; Sequence 29125, Application US/11266748A  
 ; Publication No. US20060134663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hartin, Paul  
 ; APPLICANT: Johnston, Patrick  
 ; APPLICANT: Mulligan, Karl  
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and Methods of Using the Same  
 ; TITLE OF INVENTION: Methods of Using the Same  
 ; FILE REFERENCE: 55815-0102 (319189)  
 ; CURRENT APPLICATION NUMBER: US/11/266,748A  
 ; CURRENT FILING DATE: 2005-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105479.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105482.6  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105483.4  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105507.0  
 ; PRIOR FILING DATE: 2004-11-03  
 ; APPLICANT: Caihns,Belinda  
 ; APPLICANT: Chen,Ruihuan

RESULT 14  
 US-11-248-718-73  
 ; Sequence 73, Application US/11248718  
 ; Publication No. US20060160997A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Caihns,Belinda  
 ; APPLICANT: Chen,Ruihuan

; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 0410484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 29125  
; LENGTH: 2775  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-29125

Query Match 44.1%; Score 15; DB 8; Length 2775;  
Best Local Similarity 73.3%; Pred. No. 11;  
Matches 11; Conservative 4; Mismatches 0; Indels 0;  
Gaps 0;

QY	6	ACUGAUGAGCCGUUC 20
Db	804	:  :     ::  ACTGATGAGCCGTC 818

Search completed: August 28, 2006, 10:07:13  
Job time : 781 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using SW model  
Run on: August 28, 2006, 09:45:17 ; Search time 2332 Seconds  
815.290 Million cell updates/sec

Title: US-09-847-601B-100

Perfect score: 34  
Sequence: 1 ugcacaaacugauagccguucggcgaaacgaaag 34

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_htc:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_gsb1:\*
- 12: gb\_gsb2:\*
- 13: gb\_gsb3:\*
- 14: gb\_gsb4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

#### ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	19	52.9	CZB20350	RESULT 1
2	18	52.9	AV681631	CZB20350 LOCUS C2B20350 311 bp DNA linear GSS 26-JUL-2005 DEFINITION Ba0198H18.r OC__Ba Oryza coarctata genomic clone OC__Ba0198H18 3', genomic survey sequence.
3	18	52.9	CZB202927	ACCESSION C2B20350 VERSION C2B20350.1 GI:71260203 KEYWORDS GSS.
4	18	52.9	CZB20348	SOURCE Oryza coarctata (Porteresia coarctata) - ORGANISM Oryza coarctata
5	18	52.9	CZB04464	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoidae; Oryzeae; Oryza.
6	18	52.9	CZB78533	TITLE OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
7	17	50.0	DUB08944	REFERENCE Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D., Wing,R., Rao,K., Luo,M., Jetty,R., Kudrna,D., Miller,C., Soderlund,C. and Wang,X. (2005) Unpublished (2005)
8	17	50.0	DUB08944	AUTHORS Contact: Rod A. Wing
9	17	50.0	DUB0702	JOURNAL Title: 520 626 9595
10	17	50.0	DX010184	Fax: 520 621 1259
11	17	50.0	DX20906	Email: rwting@genome.arizona.edu
12	17	50.0	DY28987	PCR Primers FORWARD: TAA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA
13	17	50.0	DY759053	Plate: 0198 row: H column: 18
14	17	50.0	DY692115	Seq primer: CAC TCA TTA GGC ACC CCA
15	17	47.1	BW68335	Class: BAC ends
16	16	47.1	BW68335	FEATURES Location/Qualifiers
17	16	47.1	BW85921	1. .311 /organism="Oryza coarctata"
18	16	47.1	N71828	/mol_type="genomic DNA", /db_xref="taxon:77588", /clone="OC__Ba0198H18", /tissue_type="leaves", /dev_stage="mature", /lab_host="DH10B", /clone_lib="OC__Ba"
19	16	47.1	AZ928987	
20	16	47.1	DY759053	
21	16	47.1	ASNG2280	
22	16	47.1	BW68335	
23	16	47.1	BW68335	
24	16	47.1	BW68335	
25	16	47.1	CZB20003	
26	16	47.1	CP287058	
27	16	47.1	DR140280	
28	16	47.1	AW26734	
29	16	47.1	CB832373	
30	16	47.1	AW651879	
31	16	47.1	CO023557	
32	16	47.1	CO023557	
33	16	47.1	CW929157	
34	16	47.1	DR140280	
35	15	44.1	AW626734	
36	15	44.1	CB832373	
37	15	44.1	CO023557	
38	15	44.1	CO023557	
39	15	44.1	DR140280	
40	15	44.1	AW626734	
41	15	44.1	CB832373	
42	15	44.1	CO023557	
43	15	44.1	DR140280	
44	15	44.1	AW626734	
45	15	44.1	CB832373	

## ORIGIN

/note="Vector: PAGIBACI; site\_1: HindIII; site\_2: HindIII"

SOURCE Oryza coarctata (*Porteresia coarctata*)  
ORGANISM Oryza coarctata  
Bukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
Clade; Ehrartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 579)  
Rao,K., Luu,M., Jetty,R., Kudrna,D., Miller,C., Soderlund,C. and  
Wing,R.

TITLE OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute  
JOURNAL Unpublished (2005)

COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu

## RESULT 2

Ave81631

LOCUS AV681631

DEFINITION AV681631 GKB Homo sapiens cDNA clone GKBH02 5', mRNA sequence.

ACCESSION AV681631

VERSION AV681631.1

JOURNAL GI:10283194

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 470)

AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,  
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., He,W.,  
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,  
Hu,G., Gu,J., Chen,Z., and Han,Z.

TITLE Insight into hepatocellular carcinogenesis at transcriptome level  
by comparing gene expression profiles of hepatocellular carcinoma  
with those of corresponding noncancerous liver  
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL PUBMED

COMMENT 11752456

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203

P.R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES source

1. .470

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="GKBH02"

/tissue\_type="hepatocellular carcinoma"

/dev\_stage="Adult"

/lab\_host="SOLR"

/clone\_lib="GKB"

/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:

XbaI"

ORIGIN

Query Match

Best Local Similarity

Matches

52.9%; Score 18; DB 1; Length 470;

Pred. No. 12;

Mismatches 14;

Conservative 4;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18; DB 1; Length 311;

Pred. No. 12;

Mismatches 15;

Conservative 3;

Indels 0;

Gaps 0;

ORIGIN

Query Match

Best Local Similarity

Matches

83.3%; Score 18

		Best local similarity 83.3%; Pred. No. 13; Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
FORWARD:	TAA TAC GAC TCA CTA TAG GG	
BACKWARD:	CAC TCA TTA GGC ACC CCA	
Plate:	0198 row: H column: 17	
Seq primer:	CAC TCA TTA GGC ACC CCA	
Class:	BAC ends.	
FEATURES	Location/Qualifiers	
source		1. .532
	/organism="Oryza coarctata"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:77588"	
	/clone="OC_Ba0198H17"	
	/tissue_type="leaves"	
	/dev_stage="mature"	
	/lab_host="DH10B"	
	/clone_lib="OC_Ba"	
	/note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII"	
ORIGIN		
Query Match	52.9%; Score 18; DB 13; Length 910;	
Best Local Similarity 83.3%; Pred. No. 13; Mismatches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;		
Qy	11 UGAGCCGTTGGGGGAA 28	
Db	228 TGAGCCGTTGGGGGAA 245	
RESULT 5		
DEFINITION	C2804464 OC_Ba017B01.f OC_Ba Oryza coarctata genomic clone OC_Ba017B01	
ACCESSION	C2804464	5', genomic survey sequence.
VERSION	C2804464.1	GI:71354339
KEYWORDS	GSS.	
REFERENCE		
AUTHORS	Oryza coarctata (Porteresia coarctata)	
ORGANISM	Bukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.	
REFERENCE		
JOURNAL	Oryza coarctata (Porteresia coarctata)	
COMMENT	Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and Wing,R.	
TITLE	Oryza Map Alignment Project - Arizona Genomics Institute	
JOURNAL	Unpublished (2005)	
COMMENT	Contact: Rod A. Wing	
FEATURES	Source	
FORWARD:	TAA TAC GAC TCA CTA TAG GG	
BACKWARD:	CAC TCA TTA GGC ACC CCA	
Plate:	0280 row: C column: 17	
Seq primer:	TAA TAC GAC TCA CTA TAG GG	
Class:	BAC ends.	
FEATURES	Location/Qualifiers	
source		1. .910
	/organism="Oryza coarctata"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:77588"	
	/clone="OC_Ba2280C17"	
	/tissue_type="leaves"	
	/dev_stage="mature"	
	/lab_host="DH10B"	
	/clone_lib="OC_Ba"	
	/note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII"	
ORIGIN		
Query Match	52.9%; Score 18; DB 13; Length 660;	
Best Local Similarity 83.3%; Pred. No. 13; Mismatches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;		
Qy	11 UGAGCCGTTGGGGGAA 28	
Db	228 TGAGCCGTTGGGGGAA 245	
RESULT 6		
DEFINITION	C2878583 OC_Ba0280C17.f OC_Ba Oryza coarctata genomic clone OC_Ba0280C17	
ACCESSION	C2878583	5', genomic survey sequence.
VERSION	C2878583.1	GI:71354339
KEYWORDS	GSS.	
REFERENCE		
AUTHORS	Oryza coarctata (Porteresia coarctata)	
ORGANISM	Bukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.	
REFERENCE		
JOURNAL	1 (bases 1 to 910)	
COMMENT	Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.' and Rao,K., Luo,M., Jetty,R., Kudrna,D., Miller,C., Soderlund,C. and Wing,R.	
TITLE	Arizona Genomics Institute	
JOURNAL	Forbes Building Room 303, Tucson, AZ 85721-0036, USA	
COMMENT	Unpublished (2005)	
FEATURES	Source	
FORWARD:	TAA TAC GAC TCA CTA TAG GG	
BACKWARD:	CAC TCA TTA GGC ACC CCA	
Plate:	520 626 9595	
Seq primer:	TAA TAC GAC TCA CTA TAG GG	
Class:	BAC ends.	
FEATURES	Location/Qualifiers	
source		1. .910
	/organism="Oryza coarctata"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:77588"	
	/clone="OC_Ba2280C17"	
	/tissue_type="leaves"	
	/dev_stage="mature"	
	/lab_host="DH10B"	
	/clone_lib="OC_Ba"	
	/note="Vector: PAGIBAC1; Site_1: HindIII; Site_2: HindIII"	
ORIGIN		
Query Match	52.9%; Score 18; DB 13; Length 910;	
Best Local Similarity 83.3%; Pred. No. 13; Mismatches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;		
Qy	11 UGAGCCGTTGGGGGAA 28	
Db	437 TGAGCCGTTGGGGGAA 454	
RESULT 7		
DEFINITION	DUB08944 LOCUS OG_Aba0093B05_r OG_Aba0093B05	
ACCESSION	DUB08944	591 bp DNA linear GSS 13-DEC-2005
VERSION	DUB08944.1	GI:83604603
KEYWORDS	GSS.	
REFERENCE		
AUTHORS	Oryza granulata	
ORGANISM	Bukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta;	
COMMENT	Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta;	
Query Match	52.9%; Score 18; DB 13; Length 660;	







REFERENCE  
1 (bases 1 to 359)  
AUTHORS  
Yu, J., Holland, L.Z., Shin-i,T., Kohara, Y., Satou, Y. and Satoh, N.  
TITLE  
Expressed genes in Branchiostoma floridæ  
JOURNAL  
Unpublished (2005)  
COMMENT  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp  
If you want to have a cDNA clone for this EST or if you have any  
questions, please send an e-mail to Nori Satch  
(satch@ascidian.zool.kyoto-u.ac.jp) and its cc to yutaka Satou  
(yutaka@ascidian.zool.kyoto-u.ac.jp).

## FEATURES

## source

## 1.

.359  
/organism="Branchiostoma floridæ"  
/mol\_type="mRNA"  
/db\_xref="taxon:7739"  
/clone="bfne085\_01"  
/tissue\_type="whole animal"  
/dev\_stage="neurula"  
/clone\_lib="Ampioxus Branchiostoma floridæ unpublished  
cDNA library, neurula whole animal"

## ORIGIN

Query Match  
Best Local Similarity 93.8%; Pred. No. 1.8e+02;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 19 UCCGGGGGAACGAG 34  
Db 45 TCCGGGGGAACGAG 60

Search completed: August 28, 2006, 10:29:08  
Job time : 2336 secs

**This Page Blank (uspto)**

Copyright: GenCore version 5.1.9  
 Copyright: (c) 1993 - 2006 Biocceleration Ltd.

Om nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:45:19 ; Search time 2471 Seconds  
 (without alignments)  
 879,892 Million cell updates/sec

Title: US-09-847-601B-100

Perfect score: 34

Sequence: 1 ugcaaacngaugagccgugcggcgaaacgaa 34

Scoring table: OLIGO\_NUC

Word size : 1

Gapext 60.0 , Gapext 60.0

Total number of hits satisfying chosen parameters: 12730834

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_env:\*

2: gb\_pat:\*

3: gb\_ph:\*

4: gb\_pl:\*

5: gb\_pr:\*

6: gb\_ro:\*

7: gb\_stb:\*

8: gb\_sy:\*

9: gb\_un:\*

10: gb\_vl:\*

11: gb\_ov:\*

12: gb\_hsg:\*

13: gb\_in:\*

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES										
Result No.	Score	Query Match Length	DB ID	Description	ORIGIN	FEATURES	SOURCE	ALIGMENTS		
1	34	100.0	34	AR408007 Sequence	RESULT 1					
2	27	79.4	32	AR408008 Sequence	AR408007 LOCUS	AR408007 DEFINITION	AR408007 ACCESSION	AR408007 VERSION	AR408007.1 GI:40157994	
3	27	79.4	34	2 AR408005 Sequence	AR408008 KEYWORDS	Sequence 100 from patent	34 bp RNA	RNA	linear	PAT 18-DEC-2003
4	26	76.5	34	2 AR407999 Sequence	SOURCE	AR408007.1	US 6632057.			
5	26	76.5	34	2 AR408000 Sequence	ORGANISM	Unknown.				
6	26	76.5	34	2 AR408006 Sequence	REFERENCE	Unclassified.				
7	25	73.5	34	2 BD263835 Adeno-ss	AUTHORS	1 (bases 1 to 34)				
8	25	73.5	34	2 AR407997 Sequence	TITLE	Fauchet,C.R.J.				
9	25	73.5	34	2 AR407998 Sequence	JOURNAL	Fixing unit with an end imprint in a threaded terminal portion				
10	25	73.5	34	2 AR408002 Sequence	FRX;	Patent: US 6632057-A 100 14-OCT-2003;				
11	25	73.5	34	2 AR408003 Sequence	FEATURES	GFI Aerospace; Paris;				
12	25	73.5	34	2 AR408004 Sequence	SOURCE	Location/Qualifiers				
13	25	73.5	34	2 AR408021 Sequence	1. .34	1. /organism="unknown" /mol_type="unassigned RNA"				
14	25	73.5	34	2 BD263871 Adeno-ss	ORIGIN					
15	25	73.5	34	2 AX048357 Sequence	Qy	1 UGCAACATGAGCCCTUCCGGCGAACGAG 34				
16	24	70.6	34	2 BD263833 Adeno-ss	Db	1 TGCACAACTGATGAGCCCTUCCGGCGAACGAG 34				
17	24	70.6	34	2 BD263837 Adeno-ss	RESULT 2					
18	24	70.6	34	2 BD263839 Adeno-ss	AR408008 LOCUS	AR408008 DEFINITION	AR408008 ACCESSION	AR408008 VERSION	AR408008.1 GI:40157995	
19	24	70.6	34	2 BD263870 Adeno-ss	AR408008 Sequence	Sequence 101 from patent	32 bp RNA	RNA	linear	PAT 18-DEC-2003
20	24	70.6	34	2 BD263873 Adeno-ss	BD263870 Adeno-ss	BD263873 Adeno-ss	BD263873 Adeno-ss	Adeno-ss	Adeno-ss	
21	24	70.6	35	2 BD263874 Adeno-ss	BD263873 Adeno-ss	BD263874 Adeno-ss	BD263874 Adeno-ss	Adeno-ss	Adeno-ss	
22	24	70.6	35	2 BD263875 Adeno-ss	BD263874 Adeno-ss	BD263875 Adeno-ss	BD263875 Adeno-ss	Adeno-ss	Adeno-ss	
23	24	70.6	35	2 BD263876 Adeno-ss	BD263875 Adeno-ss	BD263876 Adeno-ss	BD263876 Adeno-ss	Adeno-ss	Adeno-ss	
24	24	70.6	35	2 AX048356 Sequence	AX048355 Sequence	AX048356 Sequence	AX048356 Sequence	Sequence	Sequence	
25	24	70.6	35	2 AX048301 Sequence	AX048301 Sequence	AX048301 Sequence	AX048301 Sequence	Adeno-ss	Adeno-ss	
26	24	70.6	36	2 BD263870 Adeno-ss	BD263870 Adeno-ss	BD263870 Adeno-ss	BD263870 Adeno-ss	Adeno-ss	Adeno-ss	
27	24	70.6	36	2 BD263874 Adeno-ss	BD263874 Adeno-ss	BD263874 Adeno-ss	BD263874 Adeno-ss	Adeno-ss	Adeno-ss	
28	24	70.6	36	2 BD263875 Adeno-ss	BD263875 Adeno-ss	BD263875 Adeno-ss	BD263875 Adeno-ss	Adeno-ss	Adeno-ss	
29	24	70.6	36	2 AX048356 Sequence	AX048355 Sequence	AX048356 Sequence	AX048356 Sequence	Sequence	Sequence	
30	24	70.6	36	2 AX048360 Sequence	AX048359 Sequence	AX048360 Sequence	AX048360 Sequence	Adeno-ss	Adeno-ss	
31	24	70.6	36	2 AX048362 Sequence	AX048361 Sequence	AX048362 Sequence	AX048362 Sequence	BD263869 Adeno-ss	BD263869 Adeno-ss	
32	24	70.6	44	2 BD263873 Adeno-ss	BD263873 Adeno-ss	BD263873 Adeno-ss	BD263873 Adeno-ss	Adeno-ss	Adeno-ss	
33	24	70.6	44	2 BD263874 Adeno-ss	BD263874 Adeno-ss	BD263874 Adeno-ss	BD263874 Adeno-ss	Adeno-ss	Adeno-ss	
34	24	70.6	44	2 BD263875 Adeno-ss	BD263875 Adeno-ss	BD263875 Adeno-ss	BD263875 Adeno-ss	Adeno-ss	Adeno-ss	
35	24	70.6	44	2 AX048355 Sequence	AX048354 Sequence	AX048355 Sequence	AX048355 Sequence	Sequence	Sequence	
36	24	70.6	44	2 AX048359 Sequence	AX048358 Sequence	AX048359 Sequence	AX048359 Sequence	Adeno-ss	Adeno-ss	
37	24	70.6	44	2 AX048361 Sequence	AX048360 Sequence	AX048361 Sequence	AX048361 Sequence	BD263869 Adeno-ss	BD263869 Adeno-ss	
38	19	55.9	34	2 AR408001 Sequence	AR408001 Sequence	AR408001 Sequence	AR408001 Sequence	Adeno-ss	Adeno-ss	
39	18	52.9	34	4 AY09463 Lactoris	AY09463 Lactoris	AY09463 Lactoris	AY09463 Lactoris			
40	18	52.9	3322	4 AV292898 Lactoris	AV292898 Lactoris	AV292898 Lactoris	AV292898 Lactoris			
41	18	52.9	110000	15 BR000940_00	BR000940_00	BR000940_00	BR000940_00			
42	17	50.0	2198	13 AY521789 Gongylius	AY491217 Gongylius	AY491217 Gongylius	AY491217 Gongylius			
43	17	50.0	4039	15 AR425991 Streptomyces	AY521789 Gongylius	AY521789 Gongylius	AY521789 Gongylius			
44	17	50.0	110000	15 CP000124_11 Continuation (12 o	CP000124_11 Continuation (12 o	CP000124_11 Continuation (12 o	CP000124_11 Continuation (12 o			

REFERENCE 1 (bases 1 to 32)  
 AUTHORS Fauchet,C.R.J.  
 TITLE Fixing unit with an end imprint in a threaded terminal portion  
 JOURNAL Patent: US 6632057-A 101 14-OCT-2003;  
 GFI Aerospace; Paris;  
 FRX;  
 FEATURES Source  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

ORIGIN

Query Match 79.4%; Score 27; DB 2; Length 32;  
 Best Local Similarity 85.2%; Pred. No. 7.7e-06;  
 Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAUGAGCCGCUUCGGCGAAC 30  
 Db 5 AACTGATGAGCCGTTCCGGCGAAC 30

RESULT 5  
 AR408000 AR408000  
 LOCUS Sequence 93 from patent US 6632057.  
 DEFINITION 34 bp RNA  
 ACCESSION AR408000  
 VERSION AR408000.1 GI:40157987  
 KEYWORDS ·  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 34)  
 AUTHORS Fauchet,C.R.J.  
 TITLE Fixing unit with an end imprint in a threaded terminal portion  
 JOURNAL Patent: US 6632057-A 93 14-OCT-2003;  
 GFI Aerospace; Paris;

FEATURES Source  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

ORIGIN

Query Match 79.4%; Score 27; DB 2; Length 34;  
 Best Local Similarity 85.2%; Pred. No. 7.6e-06;  
 Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAUGAGCCGCUUCGGCGAAC 31  
 Db 5 AACTGATGAGCCGTTCCGGCGAAC 31

RESULT 6  
 AR408006 AR408006  
 LOCUS Sequence 99 from patent US 6632057.  
 DEFINITION 34 bp RNA  
 ACCESSION AR408006  
 VERSION AR408006.1 GI:40157993  
 KEYWORDS ·  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 34)  
 AUTHORS Fauchet,C.R.J.  
 TITLE Fixing unit with an end imprint in a threaded terminal portion  
 JOURNAL Patent: US 6632057-A 99 14-OCT-2003;  
 GFI Aerospace; Paris;

FEATURES Source  
 /organism="unknown"  
 /mol\_type="unassigned RNA"

ORIGIN

Query Match 76.5%; Score 26; DB 2; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 3.4e-05;  
 Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAUGAGCCGCUUCGGCGAAC 30  
 Db 5 AACTGATGAGCCGTTCCGGCGAAC 30

RESULT 7

BD263835	BD263835	34 bp RNA linear PAT 17-JUL-2003		
DEFINITION	Adeno-associated virus-delivered ribozyme compositions and methods of use.			
ACCESSION	BD263835			
VERSION	BD263835.1 GI:33073603			
KEYWORDS	JP 2002542805-A/57;			
SOURCE	synthetic construct			
ORGANISM	other sequences; artificial sequences.			
REFERENCE	1 (bases 1 to 34)			
AUTHORS	Burger,C.			
TITLE	Adeno-associated virus-delivered ribozyme compositions and methods of use			
JOURNAL	PATENT: JP 2002542805-A 57 17-DEC-2002;			
COMMENT	UNIVERSITY OF FLORIDA OS Artificial Sequence			
PN	JP 2002542805-A/57			
PD	17-DEC-2002			
PP	28-APR-2000 JP 2000015402			
PR	30-APR-1999 US 60/131942			
FT	PI ALFRED S LEWIN, NICHOLAS MUZYCKA, WILLIAM W HAUSWIRTH PI			
FT	'CHRISTIAN TESCHENDORF, PI CORINNA BURGER			
PC	C12N15/09,A01K67/027,C12N9/00-C12Q1/68,C12N15/00 CC Description of Artificial Sequence: SYNTHETIC PEPTIDE FR Key			
Qy	6 ACTCGAUGAGCCGTTUCGGCGGAAC 30			
FEATURES	Location/Qualifiers			
Source	1. .34 /organism='Artificial Sequence'. 1. .34 /organism='Synthetic construct' /mol_type="genomic RNA" /db_xref="taxon:32630"			
ORIGIN				
Query Match	Best Local Similarity 84.0%; Pred. No. 0.00015; Mismatches 0; Indels 0; Gaps 0;			
Matches	21; Conservative			
Db	6 ACTGATGAGCCGTTTCGGCGGAAC 30			
RESULT 8				
AR407997	AR407997	34 bp RNA linear PAT 18-DEC-2003		
LOCUS	Sequence 90 from patent US 6632057.			
DEFINITION	Fixing unit with an end imprint in a threaded terminal portion			
ACCESSION	AR407997			
VERSION	AR407997.1 GI:40157984			
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 34)			
AUTHORS	Fauchet,C.R.J.			
TITLE	Fixing unit with an end imprint in a threaded terminal portion			
JOURNAL	PATENT: US 6632057-A 95 14-OCT-2003; GPI Aerospace; Paris; FRX;			
FEATURES	Location/Qualifiers			
Source	1. .34 /organism="unknown" /mol_type="unassigned RNA"			
ORIGIN				
Query Match	Best Local Similarity 84.0%; Pred. No. 0.00015; Mismatches 0; Indels 0; Gaps 0;			
Matches	21; Conservative			
Db	6 ACTCGAUGAGCCGTTTCGGCGGAAC 30			
RESULT 11				
AR408003	AR408003	34 bp RNA linear PAT 18-DEC-2003		
LOCUS	Sequence 96 from patent US 6632057.			
DEFINITION				
ACCESSION	AR408003			
VERSION	AR408003.1 GI:40157990			
KEYWORDS				
SOURCE				
ORIGIN				
Query Match	Best Local Similarity 84.0%; Pred. No. 0.00015; Mismatches 0; Indels 0; Gaps 0;			
Matches	21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;			
Db	6 ACTCGAUGAGCCGTTTCGGCGGAAC 30			



REFERENCE  
AUTHORS  
Lewin,A.S., Muzychka,N., Hauswirth,W.W., Teschendorf,C. and  
Burger,C.  
TITLE  
Adeno-associated virus-delivered ribozyme compositions and methods  
of use  
PATENT: WO 0067780-A 93 09-NOV-2000;  
University of Florida (US)  
FEATURES  
Source  
1. .44  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/notes="SYNTHETIC OLIGONUCLEOTIDE"

ORIGIN

Query Match 73.5%; Score 25; DB 2; Length 44;  
Best Local Similarity 84.0%; Pred. No. 0.00015; O; Gaps 0;  
Matches 21; Conservatve 4; Mismatches 0; Indels 0;  
QY 6 ACUGAUGAGCCGUUCGGCGGAAAC 30  
DB 11 ACTGATGAGCCGTCGCCGAAC 35

Search completed: August 28, 2006, 10:26:44  
Job time : 2472 secs

This Page Blank (uspto,